

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 16, 2004, 11:08:12 ; Search time 49 seconds  
(without alignments)  
1586.865 Million cell updates/sec

Title: US-10-018-672-2  
Perfect score: 1383  
Sequence: 1 MNEFKINGICALASGIALAG.....TDEVEAEAKQFDGVKGVKGV 276

Scoring table: BLOSUM62  
Gap 10.0, Gapext 0.5

Searched: 1158786 seqs, 281726120 residues

Total number of hits satisfying chosen parameters: 1158786

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Published Applications AA:

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1368	98.9	276	12 US-10-282-122A-63386	Sequence 63386, A
2	1007.5	72.8	273	12 US-10-380-817-2	Sequence 2, Appli
3	1007.5	72.8	273	12 US-10-380-817-4	Sequence 4, Appli
4	1007.5	72.8	273	12 US-10-380-817-8	Sequence 8, Appli
5	1007.5	72.8	273	12 US-10-380-817-10	Sequence 10, Appli
6	1006.5	72.8	273	9 US-09-815-242-11067	Sequence 11067, A
7	1006.5	72.8	273	12 US-10-282-122A-58240	Sequence 58240, A
8	1006.5	72.8	273	12 US-10-380-817-6	Sequence 6, Appli
9	888	64.2	276	12 US-10-282-122A-67387	Sequence 67387, A
10	793.5	57.4	271	12 US-10-282-122A-76195	Sequence 76195, A
11	782.5	56.6	271	9 US-09-815-242-10050	Sequence 10050, A
12	782.5	56.6	271	12 US-10-282-122A-43291	Sequence 43291, A
13	780.5	56.4	271	12 US-10-282-122A-55826	Sequence 55826, A
14	775.5	55.1	271	12 US-10-282-122A-59600	Sequence 59600, A
15	757.5	54.8	271	12 US-10-282-122A-68391	Sequence 68391, A

16	757.5	54.8	271	12 US-10-282-122A-78174	Sequence 78174, A
17	751.5	54.3	275	12 US-10-282-122A-77174	Sequence 77174, A
18	743.5	53.8	240	9 US-09-815-242-11656	Sequence 11656, A
19	562	40.6	295	12 US-10-282-122A-47704	Sequence 47704, A
20	551	39.8	262	12 US-10-282-122A-51371	Sequence 51371, A
21	549.5	39.7	272	12 US-10-282-122A-50375	Sequence 50375, A
22	545	39.4	256	12 US-10-282-122A-61127	Sequence 61127, A
23	540	39.0	268	12 US-10-282-122A-49256	Sequence 49256, A
24	527.5	38.1	270	12 US-10-282-122A-49339	Sequence 49339, A
25	526.5	38.1	265	12 US-10-282-122A-51201	Sequence 51201, A
26	506.5	36.6	261	12 US-10-282-122A-67692	Sequence 67692, A
27	502.5	36.3	260	9 US-09-815-242-12110	Sequence 12110, A
28	502.5	36.3	260	12 US-10-282-122A-66844	Sequence 66844, A
29	497.5	36.0	259	9 US-09-815-242-5146	Sequence 5146, Ap
30	497.5	36.0	259	12 US-10-282-122A-43469	Sequence 43469, A
31	494	35.7	263	12 US-10-282-122A-52376	Sequence 52376, A
32	488	35.3	256	12 US-10-282-122A-67627	Sequence 67627, A
33	487	35.2	257	12 US-10-282-122A-69359	Sequence 69359, A
34	481	34.8	277	12 US-10-282-122A-57209	Sequence 57209, A
35	481	34.8	277	12 US-10-206-576-30	Sequence 30, Appl
36	477.5	34.5	257	12 US-10-282-122A-54418	Sequence 54418, A
37	472.5	34.2	270	12 US-10-282-122A-52496	Sequence 52496, A
38	472	34.1	270	12 US-10-282-122A-52838	Sequence 52838, A
39	468	33.8	256	12 US-10-282-122A-54417	Sequence 54417, A
40	467.5	33.8	271	9 US-09-815-242-11460	Sequence 11460, A
41	467.5	33.8	271	12 US-10-282-122A-59034	Sequence 59034, A
42	462.5	33.4	271	9 US-09-815-242-11624	Sequence 11624, A
43	462.5	33.4	271	12 US-10-335-977-4882	Sequence 4882, Ap
44	462.5	33.4	271	12 US-10-335-977-4883	Sequence 4883, Ap
45	462.5	33.4	273	12 US-10-282-122A-60558	Sequence 60558, A

check pricing for New 102(e) Jul 05/05 101

## RESULT 1

US-10-282-122A-63386  
; Sequence 63386, Application US/10282122A  
; Publication No: US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Lianguo  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636

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OM protein - protein search, using sw model

Run on: June 16, 2004, 11:00:51 ; Search time 18 Seconds  
(without alignments)  
798.409 Million cell updates/sec

Title: US-10-018-672-2

Perfect score: 1383

Sequence: 1 MNFGKINGICALASGIALAG.....TDEVEAAKKQKDGVIKGW 276

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141691 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141691

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1012.5	73.2	277	1 PLPA_PASHA	Q08868 pasteurella
2	1006.5	72.8	273	1 METQ_HAEN	P31728 haemophilus
3	888	64.2	276	1 METQ_PASU	Q9ck95 pasteurella
4	793.5	57.4	271	1 METQ_SALTI	Q82932 salmonella
5	792.5	57.3	271	1 METQ_SALTY	Q82931 salmonella
6	791.5	57.2	263	1 PLPC_PASHA	Q08870 pasteurella
7	791.5	57.2	271	1 METQ_ECO57	Q8x8v5 escherichia
8	782.5	56.6	271	1 METQ_ECOLI	P28635 escherichia
9	773	55.9	276	1 PLPB_PASHA	Q08869 pasteurella
10	757.5	54.8	271	1 METQ_YERPE	Q82h40 versinia pe
11	751.5	54.3	269	1 METQ_VIRCH	Q9ktj7 vibrio chol
12	691.5	50.0	272	1 NLPA_ECOLI	P04846 escherichia
13	686.5	49.6	272	1 NLPA_ECO57	Q8xc50 escherichia
14	416.5	30.1	268	1 TP32_TREPA	Q07950 treponema p
15	296	21.4	263	1 YHCJ_BACSU	P54594 bacillus su
16	112.5	8.1	2867	1 RBP2_PLAVD	Q00799 plasmodium
17	106	7.7	1592	1 RFP2_STRDO	P27470 streptococ
18	104.5	7.6	991	1 SCMA_EICAU	Q2aj64 rickettsia
19	103.5	7.5	543	1 CH60_MYGE	P47632 mycoplasma
20	103	7.4	1597	1 GTF1_STRDO	P11001 streptococ
21	99.5	7.2	465	1 APEA_CLOAB	Q97K30 clostridium
22	99	7.2	814	1 SLAI_BACAA	P49051 bacillus an
23	99.5	7.2	928	1 HXA2_HAEN	P45354 haemophilus
24	98.5	7.1	459	1 TME_CLOTE	C89942 clostridium
25	98	7.1	469	1 Y889_MERJA	Q58239 methanococ
26	97.5	7.0	306	1 OFBC_BACSU	Q45462 bacillus su
27	97.5	7.0	1164	1 BAG_STRAG	P27951 streptococ
28	97	7.0	1036	1 Y414_MYCCE	P47653 mycoplasma
29	96.5	7.0	339	1 PUR5_OCEIH	Q8es94 oceanobacil
30	96.5	7.0	2144	1 GLT1_YEAST	Q12680 saccharomyc
31	96	6.9	382	1 VATC_HUMAN	P21283 homo sapien
32	96	6.9	428	1 AROA_CAMJE	P52332 campylobact
33	96	6.9	525	1 SPL_FARFA	Q05308 rareobacter

ALIGNMENTS

RESULT 1				
PLPA_PASHA				
ID	PLPA_PASHA	STANDARD;	PRT;	277 AA.
AC	Q08868; Q07363;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Outer membrane lipoprotein 1 precursor (PLP1).			
GN	PLPA.			
OS	Pasteurella haemolytica.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;			
OC	Pasteurellaceae; Mannheimia.			
OX	NCBI_TaxID=75985;			
RN	[1]_			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=serotype A1;			
RX	MEDLINE=93328110; PubMed=8335249;			
RA	Murphy G.L., Whitworth L.C.;			
RT	"Analysis of tandem, multiple genes encoding 30-kDa membrane proteins			
RT	in Pasteurella haemolytica A1.;"			
RL	Gene 129:107-111(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=serotype A1;			
RX	MEDLINE=94011378; PubMed=8406866;			
RA	Cooney B.J., Lo R.Y.C.;			
RT	"Three contiguous lipoprotein genes in Pasteurella haemolytica A1			
RT	which are homologous to a lipoprotein gene in Haemophilus influenzae			
RT	type b.;"			
RL	Infect. Immun. 61:4682-4688(1993).			
CC	-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid			
CC	anchon (Probable).			
CC	-!- SIMILARITY: Belongs to the nlpa lipoprotein family.			
CC	This SWISS-PROT entry is copyright. It is produced through a collabor			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstat			
CC	the European Bioinformatics Institute. There are no restrictions on			
CC	use by non-profit institutions as long as its content is in no			
CC	modified and this statement is not removed. Usage by and for comm			
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/anno">http://www.isb-sib.ch/anno</a>			
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			
DR	EMBL; L11037; AAA25538.1; -			
DR	EMBL; M91072; AAA25541.1; -			
DR	EMBL; L16627; AAA25546.1; -			
DR	PIR; JN0751; JN0751.			
DR	InterPro; IPR004872; Lipoprotein_9.			
DR	InterPro; IPR000437; Prok_lipoprot_9.			
DR	Pfam; PF03180; Lipoprotein_9; 1.			
DR	TIGRfams; TIGR00363; TIGR00363; 1.			
DR	PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.			
KW	Outer membrane; Lipoprotein; Signal; Multigene family; Palmitate.			
FT	SIGNAL 1 19			
FT	CHAIN 20 277			
FT	LIPID 20 20			
FT	N-palmitoyl cysteine (Probable).			

Q8gb4 azotobacter  
Q05022 saccharomyc  
O67494 aquifex ae  
P96786 halicobacte  
Q9aj81 rickettsia  
P44596 haemophilus  
Q92193 mus musculus  
Q91kg7 astragalus  
Q02141 lactococcus  
Q9kx5 streptomyce  
O7vlt1 prochloroco  
Q64566 rattus norv

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OM protein - protein search, using sw model

Run on: June 16, 2004, 11:05:36 ; Search time 22 Seconds  
(without alignments)  
647.671 Million cell updates/sec

Title: US-10-018-672-2  
Perfect score: 1383  
Sequence: 1 MFNGKINGICALASGIALAG.....TDEVEAEAKKQFKDGVKGM 276

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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5: /cgn2\_6/ptodata/2/iaa/PCTUS-COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	775.5	56.1	289	4	US-09-489-039A-12337
2	757.5	54.8	279	4	US-09-543-681A-6534
3	685.5	49.6	285	4	US-09-489-039A-10541
4	671.5	48.6	279	4	US-09-543-681A-4548
5	651.5	47.1	272	4	US-09-489-039A-10410
6	596	43.1	279	4	US-09-543-681A-6914
7	520	37.6	118	4	US-09-540-236-2991
8	503.5	36.4	306	4	US-09-252-991A-18873
9	494.5	35.8	271	4	US-09-252-991A-20200
10	481	34.8	277	4	US-09-071-035-30
11	481	34.8	278	4	US-09-134-000C-4965
12	475	34.3	269	4	US-09-543-681A-4774
13	462	33.4	257	4	US-09-071-035-32
14	449.5	32.5	291	4	US-09-107-532A-7234
15	441	31.9	288	4	US-09-134-001C-4005
16	416	30.1	280	4	US-08-956-171E-5195
17	373.5	27.0	279	4	US-09-107-532A-6443
18	366	26.5	269	4	US-09-134-001C-4878
19	364	26.3	296	4	US-09-328-352-6924
20	364	26.3	326	4	US-09-489-039A-9512
21	358.5	25.9	261	4	US-09-634-238-420
22	356	25.7	260	3	US-08-961-083-32
23	356	25.7	260	4	US-09-536-784-32
24	346	25.0	273	4	US-08-956-171E-5196
25	337.5	24.4	286	4	US-09-328-352-6702
26	335	24.2	304	4	US-09-328-352-7028
27	325.5	23.5	294	4	US-09-328-352-5549

28	324	23.4	272	4	US-09-071-035-22	Sequence 22, Appl
29	322	23.3	342	4	US-09-252-991A-25420	Sequence 25420, A
30	321.5	23.2	280	4	US-09-489-039A-13968	Sequence 13968, A
31	319.5	23.1	220	4	US-09-634-238-283	Sequence 283, App
32	318	23.0	251	4	US-09-071-035-24	Sequence 24, Appl
33	315.5	22.8	272	4	US-09-071-035-10	Sequence 10, Appl
34	308.5	22.3	253	4	US-09-071-035-12	Sequence 12, Appl
35	304.5	21.8	278	4	US-09-134-000C-5006	Sequence 5006, Ap
36	257.5	18.6	275	4	US-09-198-452A-291	Sequence 291, App
37	209	15.1	306	4	US-09-489-039A-10023	Sequence 10023, A
38	108	7.8	91	4	US-09-134-000C-3687	Sequence 3687, Ap
39	106	7.7	347	4	US-09-328-352-6764	Sequence 6764, Ap
40	105	7.6	794	4	US-09-134-000C-5518	Sequence 5518, Ap
41	103	7.4	503	4	US-09-071-035-360	Sequence 360, App
42	103	7.4	1074	4	US-09-071-035-358	Sequence 358, App
43	103	7.4	1074	4	US-09-071-035-394	Sequence 394, App
44	103	7.4	1096	4	US-09-134-000C-5764	Sequence 5764, Ap
45	102.5	7.4	308	4	US-09-134-001C-4400	Sequence 4400, Ap

ALIGNMENTS

RESULT 1  
US-09-489-039A-12337  
; Sequence 12337, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 12337  
; LENGTH: 289  
; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-12337

Query Match	56.1%;	Score	775.5;	DB 4;	Length	289;
Best Local Similarity	55.2%;	Pred.No.	3.3e-73;			
Matches	153;	Conservative	45;	Mismatches	68;	Indels 11; Gaps 3;
QY	2	NFGKINGICALASGIALAGCSNQSNPEAAISKTAAQTIKVGMAGPQOAVAEVAGQVAKE	61			
Db	22	NFTFAAVGALITGSLALVCGGQDEKDP-----NHIKVGVIAGAEQQAQVAKE	73			
QY	62	KYNLTVELVEFNDYAMPNSAVSKGELDANAMQHPYLEKDSOEKGLNMLVIVGNTFVYPL	121			
Db	74	KGLDVELVTFNDYVLPNEALSKGIDIDVNAFQHKPYLDQIKDRGY-KLVAVGNTFVYPI	132			
QY	122	AGYSTKIKTLNELKDGATIAVPNDPSNLARALILEKQGLIKLKQNTLNFSTTLDIVENP	181			
Db	133	AGYSKKIKSLDELQPSQIAVPNDPTNLGRSLILLQQVGLIKLKGVGLLFTSLDIVENP	192			
QY	182	KGLVIKEVDVTSAAARID--VDLAVANNYAGOVGLTASENGVFEVDKDSYVNNIIVAR	239			
Db	193	KNLKIVELSEAPQLPSRLDDAQIALAVINTTASQIGLTPAKOGIFVEGKESPYVNNLIIVAR	252			
QY	240	ADNKSKAIQDFVKAYQYOTDEVEAEAKQFKDGVKGM	276			
Db	253	EDNKAENVKVFQAYQSDVEVEAANKIFNGGAVKGM	289			

RESULT 2  
US-09-543-681A-6534  
; Sequence 6534, Application US/09543681A  
; Patent No. 6605709  
; GENERAL INFORMATION:



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OM protein/- protein search, using sw model

Run on: June 16, 2004, 11:00:16 ; Search time 60 Seconds  
(without alignments)  
1299.719 Million cell updates/sec

Title: US-10-018-672-2

Perfect score: 1383

Sequence: 1 MNFKINGICALASGIALAG.....TDEVEAPKQKQGVKIGW 276

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_29Jan04.\*

- 1: Geneseq1980s.\*
- 2: Geneseq1990s.\*
- 3: Geneseq2000s.\*
- 4: Geneseq2001s.\*
- 5: Geneseq2002s.\*
- 6: Geneseq2003as.\*
- 7: Geneseq2003bs.\*
- 8: Geneseq2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1383	100.0	276	4	AAB20104
2	1368	98.9	276	5	AAO17582
3	1368	98.9	276	6	ABU35462
4	1007.5	72.8	273	5	ABB76073
5	1006.5	72.8	273	4	AAU35474
6	1006.5	72.8	273	5	ABB76074
7	1006.5	72.8	273	6	ABU30316
8	1004	72.6	272	5	AAO17813
9	888	64.2	276	6	ABU39463
10	793.5	57.4	271	6	ABU48271
11	782.5	56.6	271	4	AAU34457
12	782.5	56.6	271	6	ABU15367
13	780.5	56.4	271	6	ABU27902
14	775.5	56.1	271	6	ABU31676
15	767.5	55.5	272	6	ABM67576
16	757.5	54.8	271	6	ABU50250
17	757.5	54.8	271	6	ABU40467
18	751.5	54.3	275	6	ABU49250
19	743.5	53.8	240	4	AAU36063
20	562	40.6	295	6	ABU19780
21	551	39.8	262	6	ABU23447
22	549.5	39.7	272	6	ABU22451
23	545	39.4	256	6	ABU33203
24	540	38.0	268	6	ABU21332
25	527.5	38.1	270	6	ABU21415

N/C  
- N/C

## ALIGNMENTS

### RESULT 1

AAB20104

ID AAB20104 standard; protein; 276 AA.

XX AAB20104;

XX AC AAB20104;

XX DT 23-APR-2001 (first entry)

XX DE Moraxella catarrhalis BASB111 protein.

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Abu23277 Protein e  
Abu53625 Lactococ  
Abu39768 Protein e  
Abu36517 Pseudom  
Abu38920 Protein e  
Abu33650 Pseudom  
Abu15545 Protein e  
Abu25052 Protein e  
Abu29703 Protein e  
Abu41435 Protein e  
Aay00024 Enterococ  
Abp43243 E faecal  
Abu88271 E. faecal  
Abu29285 Protein e  
Abu13522 Enterococ  
Abu26494 Protein e  
Abu24572 Protein e  
Abu24914 Protein e  
Abu26493 Protein e  
Aaw90023 Expressed

26 526.5 38.1 265 6 ABU23277  
27 509.5 36.8 286 5 ABU53625  
28 506.5 36.6 261 6 ABU39768  
29 502.5 36.3 260 4 AAU36517  
30 502.5 36.3 260 6 ABU38920  
31 497.5 36.0 259 4 AAU33650  
32 497.5 36.0 259 6 ABU15545  
33 494 35.7 263 6 ABU25052  
34 488 35.3 256 6 ABU29703  
35 487 35.2 257 6 ABU41435  
36 481 34.8 277 2 AAY00024  
37 481 34.8 277 5 ABP43243  
38 481 34.8 277 6 ABU88271  
39 481 34.8 277 6 ABU29285  
40 481 34.8 277 6 ABU13522  
41 477.5 34.5 257 6 ABU26494  
42 472.5 34.2 270 6 ABU24572  
43 472 34.1 270 6 ABU24914  
44 468 33.8 256 6 ABU26493  
45 467.5 33.8 271 2 AAW90023

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